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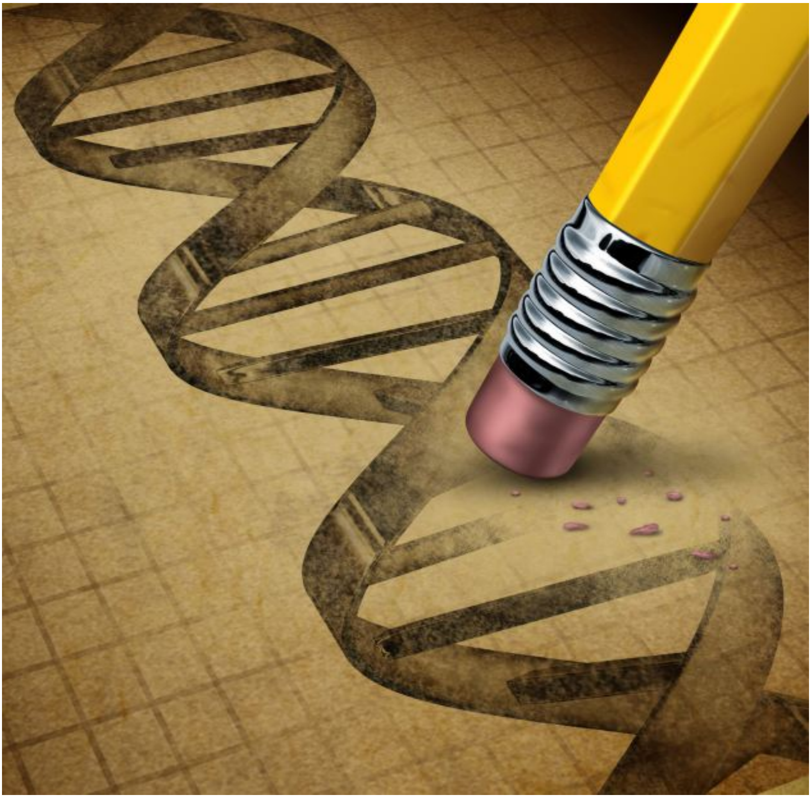
ADELPHI
GENETICS FORUM

exploring heredity and society

Adelphi Review



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EDITORIAL

This summer, I'm delighted to announce the appointment of our new President, **Professor Nicholas Wood**. He is the 26th President of our organisation dating back to the first, Sir James Crichton-Browne in 1908. Nicholas holds the UCL Chair of Genetics as well as the personal Chair in Neurogenetics and Clinical Neurology. He has been a senior lecturer, reader and professor at the Institute of Neurology, University of London since 1995.

Earlier this year, the Forum became an Organisational Member of the Royal Society of Biology. This association will have a number of important benefits for us, particularly when it comes to advertising events, grants etc. This new relationship also means that if you are a member of the Adelphi Genetics Forum, you can apply for membership of the RSB at significantly reduced rates. I recommend you have a look at their website for further details.

Planning for this year's Annual Conference is now well advanced and you can find details on page 28. The title of the conference is **Population diversity, its biological consequences and impact on disease risk**. The keynote Adelphi Lecture will be given by **Professor Stephanie Malia Fullerton**. I hope you can join us in October.

On page 4, we have latest edition of 'My Life in Genetics', featuring **Professor Nick Mascie-Taylor** who gives us some fascinating insights into his long career. We also have reports from various conferences and the final report from CHASE Africa, recipients of a significant grant from the Artemis Trust of the Adelphi Genetics Forum.

Finally, the details of the PhD studentship funded by the Forum can be found on page 26, with contributions by our Past-President, **Veronica van Heyningen** and **Dr Adam Rutherford**.

Robert Johnston

My Life in Genetics

An Interview with Professor Nick Mascie-Taylor
Trustee of the Adelphi Genetics Forum

Tell us about your early years and how your interest in genetics developed

I was born in mid Wales – Llandrindod Wells – near my mother's family home of Builth Wells but was brought up in Gloucester. I have an older brother and both of us were educated at Sir Thomas Rich's School, an old blue grammar coat. I first became interested in genetics when I was taught population genetics at university.

Which area of genetics have you been involved with in your career?

My PhD at Cambridge was in Population Genetics and I combined work on both fruit flies and humans. The head of the Genetics Department (John Thoday) was an expert on Disruptive

Selection (a specific type of natural selection that actively selects against the intermediate in a population and favours both extremes of the distribution). My work used sternopleural chaeta number in Drosophila melanogaster to see the impact of varying amounts of disruptive selection and migration between high and low sub-populations, on increase in variance and mean differences. I ran 16 selection lines and counted the number of chaetae on over 3000 flies every week! The human work involved recruiting nearly 200 Cambridge families to study social mobility and assortative mating in relation to IQ, personality and anthropometry as well as looking for associations between genetic markers (mainly blood groups) and psychometric and anthropometric variables.

I was appointed to a Lectureship in the Department of Biological Anthropology at the University of Cambridge immediately after my PhD and in that department, I taught human population genetics and biostatistics for many years. I branched out and started working on more human ecological topics in developing countries in Africa (Sudan, Kenya, Tanzania, Uganda and Zimbabwe) and Asia (Bangladesh and Nepal). When I retired from Biological Anthropology I was appointed as Director of Research in Global Health in the Department of Public Health and Primary Care at the University of Cambridge where I have been able to re-engage in more genetic related work especially through the Bangladesh Cohort study (BELIEVE, n=74,000) which is studying primarily non-communicable diseases.

Who has had the greatest influence on your work?

I think the two people who have influenced my research are Professor Geoffrey Harrison and Dr Anthony (Tony) Boyce. Geoffrey was a terrific supporter and he persuaded me to become Editor of the *Journal of Biosocial Science* ‘for 5 years’ when I was 40 years of age and I stepped down 31 years later. He also invited me to become a Trustee of The Parkes Foundation and later I took over from him as the Chairman. Tony introduced me to the delights of population genetics and biostatistics.

What do you consider to be the greatest challenges facing genetics in the coming years?

There are many, many challenges ahead! For example, efforts to find the genetic variation underlying complex human diseases has ended up explaining only a small fraction of the phenotypic variance. There are ethical issues over privacy and confidentiality of a person's own genetic information and whether testing should be compulsory. I would recommend reading Brandes et al. Genome Biology (2022) 23:131 Open problems in human trait genetics, which identifies at least 16 problems/challenges.

You've been involved with the Adelphi Genetics Forum and previously the Galton Institute for many years. What roles do you think it should play?

I think conferences on genetic-related themes are one obvious way forward such as the upcoming October 2023 meeting. Other obvious themes could be devoted to polygenic risk scores and their use in clinical settings, heritability estimates and missing heritability, and lack of ancestry diversity - individuals of non-European ancestry are heavily underrepresented and more diversity would also help deal with population structure and establish the causality of genetic associations.

Tell us one thing about yourself that isn't widely known

I have visited Bangladesh 110 times since an initial visit in December 1988 and supervised 20 PhD students from that country.

Previous contributors to the *My Life in Genetics* series:

Published in the ***Adelphi Review:***

Mr Robert Johnston	**Issue 2**
Dr Jess Buxton	**Issue 1**

Published in the ***Galton Review***:

Professor Nicholas Wood	**Issue 15**
Professor Dallas Swallow	**Issue 14**
Professor David Galton	**Issue 13**
Professor Andrew Read	**Issue 12**
Professor Veronica van Heyningen	**Issue 11**
Professor Dian Donnai	**Issue 10**
Professor Philippa Talmud	**Issue 9**

24th European Molecular Biology Laboratory PhD Symposium

The Spectra of Life – Dimensional Breadth in Biological Research

7–9 December, 2022 EMBL Heidelberg, Germany

The focus of this year's EMBL PhD symposium was biological research across different scales. To truly understand biological phenomena, it is essential to understand the interactions and coordination between the separate but inextricably interlinked spatial, temporal, systematic, and environmental contexts within which the phenomena occur. To achieve this, cooperation between experts from across different disciplines is imperative. Through this symposium we hoped to assemble and unite a diverse array of scientists, hoping to trigger fruitful discussions and exciting collaborations across disciplines to progress towards the lofty goal of advancing a holistic perspective on investigating biological systems.

This year’s symposium organising committee was composed of 33 first year PhD students from EMBL sites in Germany, France, Italy, Spain and the UK. We were thrilled to host almost 150 participants from 25 different countries spread across all continents. The symposium provided a platform to both early-stage researchers and established group leaders from a wide range of disciplines to share their research in the form of talks and poster sessions.

The conference was split into 4 sessions – Extremes, Time, Complexity and Size. Most sessions consisted of a mix of talks from keynote speakers, invited speakers and selected participants. In total we had 18 talks including 3 flash talks given by selected participants. The welcome address for the symposium was given by the Director General of EMBL **Edith Heard** who spoke about the importance of science communication as well as EMBL’s new theme of Planetary Biology. The first session titled “Extremes” saw talks from **Ikram Blilou and Elizabeth Murchinson** who delivered the EMBO Women in Science Lecture and **Buzz Baum**. Ikram presented exciting insights about how certain plant species have adapted to tough desert environments. Elizabeth shared findings on the role of horizontal gene transfer in transmissible cancers while Buzz Baum discussed the likely archaeal origin of the eukaryotic cell. In the session “Size”, **Jan Philipp Junker** from MDC Berlin gave the EMBO Young Investigator Lecture in which he spoke about the integration of temporal information in single-cell transcriptomic data and how his lab uses the same to identify mechanisms of heart regeneration. This was followed by a talk given by **Fyodor Kondrashov** from the Okinawa Institute of Science and Technology, Japan about modelling green fluorescent protein (GFP) fitness landscapes, with the brightness of a given GFP genotype serving as a fitness readout. At the end of the first day one half of the participants presented their posters and there was a networking event hosted by the sponsors.

Continuing the “Time” session on the second day, **Gerhard Hummer and Andrea Cipriano** spoke about rapid biomolecular processes such as enzymatic catalysis and how time influences epigenetic processes respectively. The third session titled “Complexity” included talks by **Prisca Liberali** from the Friedrich Miescher Institute for Biomedical Research, Switzerland, **Sandra Smit** from Wageningen University and Research, The Netherlands, and **Dennis Walsh** from the University of Toronto, Canada, who gave a refreshing philosophical perspective when considering evolutionary theories. The EMBO Keynote lecturer, **Tobias Erb** from the MPI for terrestrial microbiology, Germany shared exciting insights into harnessing natural and synthetic carbon fixation pathways. **Jean Fan** from the John Hopkins University, USA rounded out the session with an innovative discussion on the integration of multi-omics and imaging data in the context of cancer and tumour progression. The day ended with another poster session followed by a networking event.

The final session, “Size”, began on Friday morning and included two more EMBO Young Investigator lectures given by **Tanmay Bharat** about understanding the prokaryotic cell surface at the atomic level, and **Paul Guichard** looking at the structural mechanisms governing centriole assembly. This was followed by a talk by **Clarice D Aiello** that bridged physics and biology by discussing how quantum mechanics can help explain physiological biosensing phenomena. A panel discussion on ‘Inclusion and diversity in Science’ helped us understand the problems surrounding inclusivity in academia and their possible solutions. The panellists shared some personal anecdotes of their individualistic efforts of making their lab more inclusive and diverse. The panel included **Jean Fan, Elizabeth Murchison, Tanmay Bharat and Flora Vincent from** EMBL Heidelberg.

Apart from the lectures, the participants had the opportunity to attend workshops involving light sheet microscopy and research infrastructure landscape, services and FAIR data offered by Luxendo and Euro Bio-imaging respectively. The poster sessions at the end of Days 1 and 2 helped the participants to share their research with others present at the symposium. The poster prizes were awarded to **Linda Decker** from EMBL Heidelberg (Germany), **Galileo Araguirang** from University of Rostock (Germany) and **Rebecca Degnan** from The University of Queensland (Australia). Three participants were also invited to give short talks during the ‘Complexity’ session. Multiple participants were awarded travel grants as well as complete fee waivers to come and present their research.

A tour of Heidelberg city, a farewell party and numerous coffee breaks provided the participants, the organisers and the invited guests with plenty of opportunities to network, discuss and exchange ideas. The entire programme of the symposium along with details about the invited speakers can be found on the symposium website: https://phdsymposium.embl-community.io/main/#sectionLink-home

Organizing the symposium wouldn’t have been possible without the generous support of the **Adelphi Genetics Forum** and we are very grateful. The award was utilized to cover essential expenses like speaker and organizer travel, promotion, printing and event venue facilities.

Gaurav Vaidya
EMBL Heidelberg

CHASE Africa Final Report to the Artemis Trust

1 July – 31 December 2022

The last six months of 2022 saw Kenya experience its worst drought in four decades, after four consecutive rainy seasons with below average rainfall. With people in Kenya struggling to support their families' basic needs, due to high living costs, depleted resources and lack of food, CHASE Africa's sexual and reproductive health and rights services are needed more than ever. Being able to choose to bear fewer, healthier children is an especially pertinent issue in a time of severe drought.

A range of activities were carried out during the reporting period to meet our main goals of increasing demand for, and access to, quality sexual and reproductive health (SRH) services for people in Eldama Ravine. Community Health Workers (CHWs) and Youth Peer Providers (YPPs) reached out to community members through a variety of platforms, including community dialogue days, road shows, visits to tertiary institutions, world activity days (e.g. environmental day) and door-to-door outreach. YPPs provided information and referrals in a variety of social settings for young people to be able to access safe spaces for SRH services. Condoms were also distributed. Collaboration continued well with the linked health facilities, to which CHWs referred family planning clients in those regions with access to those facilities.

In regions that are too far from a health facility, family planning and other health care services were offered at four safe spaces in more accessible locations.

Outputs

The total number of people reached with SRH and family planning information was 6,362, as detailed in the table below.

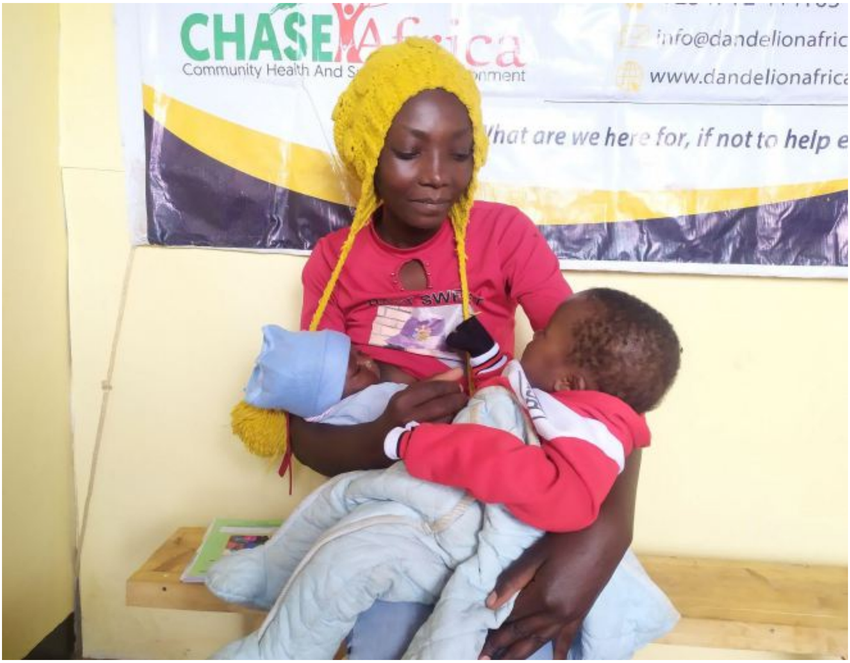
	Males	Females	Total
Aged 19 and under	828	1315	2143
Aged 20 and over	1094	3125	4219
Total	1922	4440	6362

Within the total number of people reached with information, 12 males and 12 females were living with disabilities. The total number of family planning services provided was 2,195 (equating to 3,567 couple-years of protection (CYP)), of which 1,160 recipients were first time users of contraceptives. 520 services were provided to girls aged 19 and under, and 1,675 services were provided to women aged 20 and over. Four of those women were living with disabilities. The number of people reached with family planning information during the second half of 2022 decreased in relation to the first half of the year, returning to similar numbers as reached in 2021. The reduction in numbers compared to the previous reporting period is attributed to the immense challenges households were facing due to the drought in the second half of the year, and the necessary daily requirements of finding water and food that often had to take priority over attending family planning dialogues.

The number of family planning services provided also reduced very slightly compared to the previous reporting period, however, the CYP figure increased significantly. This was due to stock shortages of several short-term family planning commodities, such as injections and pills, at the link facilities in Eldama Ravine. The unfortunate shortage of short-term contraceptives limited women’s options and meant that more women chose to try the available alternatives, which were longer-term methods, such as subcutaneous implants and intrauterine devices. The lack of access to the short-term methods resulted in some women choosing not to use contraceptives at that time, which explains the reduction in the number of family planning services provided during the reporting period. However, women who opted to receive contraceptives during this period and therefore chose longer-term methods, contributed to the increase in CYP provided compared to the previous reporting period. So, although the number of women adopting modern family planning practices was lower, each of those women who did choose to use contraceptives would be protected from pregnancy for a longer duration of time.

Many thanks for the support of the Artemis Trust of the **Adelphi Genetics Forum** for this project.

Claire Nicholls
CHASE Africa



Young mother waiting to see nurse at safe space

Nottingham Research Students' Conference in probability and statistics

4-8 September 2022

Nottingham RSC 2022 was the 45th Research Students' Conference in probability and statistics. The conference is for students and is led, run and organised by students. This year's RSC was a hybrid event in which delegates could join online (virtual delegate), in person (day delegate), or in person with accommodation (residential delegate). There were six guest speakers, as well as a discussion session, which also featured online and in-person contributions. Students presented their work to one another in smaller groups (during parallel hour-long sessions) with either a presentation or a poster, and each session was chaired by a member of the RSC organising committee. Presentations were punctuated by regular tea and coffee breaks, for delegates both to rest and to network. There were sixty delegates in total, a number similar to the Durham RSC held in 2017.

Delegates with a 4-day residential package arrived on Sunday 4th and attended a pizza night which allowed delegates to meet and connect after their (potentially lengthy!) journeys. Day delegates and 3-day residential delegates arrived on Monday 5th.

As is often the case, the first day comprised mainly of guest speakers, so that students could get comfortable at the conference before being asked to present. The head of statistics at the University of Nottingham, **Theodore Kypraios**, as well as two other guest speakers **Katie Severn** and **Stefanie Bierdermann** presented their research. In the evening, an archery event was attended by roughly 25 delegates, which received very positive feedback.

On Tuesday 6th, there were two student presentation sessions, and three further guest speakers: **Marc Deisenroth, Danielle Belgrave** and **Marcin Skwark**. A discussion on AI in healthcare allowed for delegates to debate AI and machine learning techniques, and allowed for intriguing discussion between students and speakers. Speakers received great feedback in general. On the second evening, organisers ran a pub quiz for in-person delegates, which was attended by a mix of residential and day delegates, and again received excellent feedback.

Wednesday 7th was mostly centred on student presentations; there were three such sessions. On Wednesday afternoon, those with posters presented in a session where delegates could ask questions; a few students did both a talk and a poster. Students were encouraged to vote for a best talk and best poster respectively, and small prizes were awarded for talks that were popular or were agreed to be engaging by many delegates. This was interpreted by delegates in a positive (as opposed to competitive) manner, as intended. It also allowed for further networking between delegates. For the final evening, in-person delegates and organisers attended dinner at the Orchard Hotel, in order to complete the conference.

The conference was attended by 56 students (excluding speakers) from 16 Universities across the UK and Ireland, of which 8 attended online and 48 in person and 42% of these attendees were female.

The organisers of RSC 2022 would like to thank the **Adelphi Genetics Forum** for their support of the conference. Without your contribution, some or all components of the conference would not have been possible .

Alice Thompson, Niamh Martin,
Liam Critcher, Ines Krissaane
RSC 2022 Organising Committee

Annual Meeting of the European Human Behaviour and Evolution Association

April 18-21 2023 at University College, London

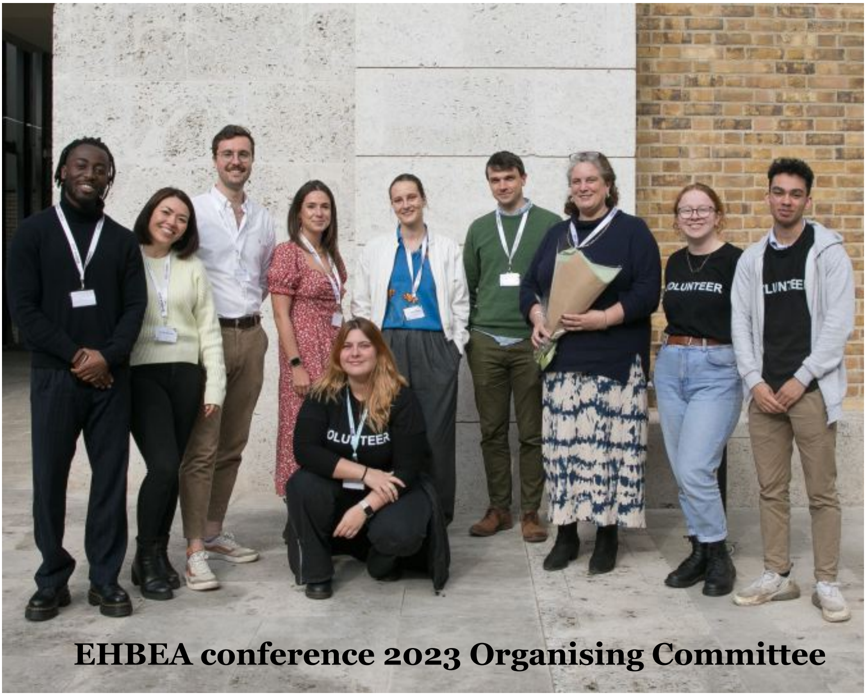
EHBEA is for anyone researching the evolution and ecology of human behaviour and culture – a topic that did not really have its own European meeting until EHBEA was established in 2008. Numbers this year were slightly higher than predicted, no doubt in part because this was the first time in three years that we have met in person due to the covid pandemic. The conference provided the first opportunity for many PhD students to present their work in person.

Plenary speakers covered the full range from cultural evolution, evolutionary anthropology, behavioural ecology and evolutionary psychology, and more. We started with a plenary from **Adam Rutherford** (Genetics, UCL) about the history of eugenics, including aspects of UCL's own chequered history in that field. Other plenaries were from **Brooke Scelza** (Anthropology, UCLA) on multiple paternity, **Khandis Blake** (Psychology, Melbourne) on sex roles, **Tim Clutton-Brock** (Zoology, Cambridge) on social evolution in mammals, **Mark Thomas** (Genetics, UCL) on the evolution of lactose tolerance and our New Investigator award plenary went to **Sheina Lew-Levy** (Anthropology, Durham) who spoke on hunter-gatherer childhood. In addition to the plenaries, we had three days of three concurrent meeting rooms keeping us all up to date in our field with over 150 presentations. At lunchtime we had some optional workshops. On Thursday, courtesy of **Reuben Fakoya-Brooks** and **Tasmin Alexander** of the REED network (working for Racial and Ethnic Equality and Diversity), we held a workshop on how to be an effective ally, which generated some good questions and lively discussion. EHBEA is not as ethnically diverse as we would like, and anything that can help is important.

On Friday, courtesy of **Rebecca Sear** and Cambridge University Press, we had a session on ‘how to get published’.

The social occasions were a very important part of the meeting too, providing an opportunity for everyone to catch up after so many years of disrupted or online only meetings and giving newcomers to the field a chance to develop their social networks. The conference ended with a ‘banquet’ that was a fantastic river cruise and dinner down the Thames. Seeing London lit up at night on a fine April evening in a beautiful paddle steamer, with plenty of space to mingle and eat, was wonderful, capped off by the opening of Tower Bridge as we passed underneath. We are extremely grateful to our sponsors, including the **Adelphi Genetics Forum**, for making this event possible. Next year we will all meet again in Montpellier.

Ruth Mace (UCL)
Chair of the organising committee EHBEA 2023


EHBEA conference 2023 Organising Committee

British Society for Population Studies

2022 Conference at the University of Winchester

Over the course of two full days, over 270 people participated, with 188 presentations in 47 sessions. There was a pleasingly large contingent of presenters from outside the UK, primarily from Europe.

The Office for National Statistics curated three sessions on Developments in Official Statistics and, in addition to the familiar strands that run at all BSPS conferences, there were sessions on Systems Science in Public Health and Health Economics Research (SIPHER); Critical demography & qualitative research; Population processes and data in crisis and conflict settings; and Demographic consequences of environment risks. There were two well-attended plenary sessions. **Professor Sir Ian Diamond**, the National Statistician, spoke about measuring populations and their characteristics: past, present and future, whilst the other plenary was a conversation between **Professor Rachel Franklin** (Newcastle University) and **Professor Andy Tatem** (University of Southampton) on the changing data ecosystem in demography: non-traditional data sources, see reports below.

For the last few years, BSPS has offered a plenary spot at the annual conference to the winner of the BSPS early career award, for which entries are solicited among the membership. This scheme is aimed at highlighting the achievements of early career researchers in population studies, who have the potential to make a significant contribution to population studies. This year’s winner was **Dr Diego Alburez Gutierrez** (Max Planck Institute for Demographic Research) who gave a fascinating talk on 'Kinequality': studies at the intersection of demography, kinship, and inequality'.

Additionally, there was a postgraduate and early career mentoring session, a mixer event where PhD and ECR attendees had the opportunity to meet demographers from academic and non-academic fields, to learn more about career opportunities, experiences navigating job markets, and more.

A lively poster session in tandem with a reception on the first evening saw a pleasing amount of interaction between presenters and attendees. There were joint winners of the poster competition: Ignacio Franco Vega from the University of Bath for 'A descriptive study of hostales in the southern cone of Lima and an assessment of their potential as sites for sexual health studies and interventions' and Mallika Snyder from the University of California at Berkeley for 'Who will remember COVID-19? Kinship memory after a global pandemic'.

Plenary reports:

Plenary session 1: The changing data ecosystem in demography. Non-traditional data sources.

Professor Rachel Franklin (Newcastle University) and Professor Andy Tatem (University of Southampton) in conversation

The first plenary session on “The changing data ecosystem in demography. Non-traditional data sources” took the form of a conversation between Professor Rachel Franklin from Newcastle University and Professor Andy Tatem from the University of

Southampton, chaired by BSPS President Professor Alice Reid. The session highlighted the emergence of new data sources (eg spatial satellite data) that can be added to and integrated with traditional individual-level data sources such as surveys and censuses to understand demographic processes.

The discussion started with ways to characterise environments, define data scales, sampling of data, and the necessity to reconstruct data assumptions, robustness checks, and model estimates. The production of census areas and the allocation of people into them was given as an example, highlighting the necessity of considering finer spatial scales. Defining spatial and temporal dimensions is needed especially that different resolutions and definitions for what is a city, what is a village exist worldwide. In this context, satellite data covering and mapping the entire world at less than 5 km spatial scales can be beneficial. Satellite spatial data can be used to observe new developments and population progress. For example, using spatial data to examine how built environment characteristics and landscape are related to demographic processes such as fertility and migration would be interesting for future research in demography.

The difference between prediction and explanation was also discussed. For example, using the chicken density (which is one of the best predictions) to predict vaccination rates in children is the first step followed by causality investigation and analysis of patterns in the existing data.

The plenary also discussed the limitations of spatial and individual-level data. The first limitation is that we cannot capture everything with a satellite and thus individual-level census data are needed to understand some patterns in the population and demography. Another issue is that satellite spatial data can be used to identify clusters and people discriminations. By linking this satellite spatial data to individual-level data including data about individual preferences from industries to produce more accurate results, information sensitivities and sharing rights emerge. For example, if individual-level data is matched to location data, there is a risk of identifying the individuals. Nevertheless, linking individual-level data to aggregated spatial data can enhance the potential of examining the underlying processes for demographic process such as migration. For example, census data can show that migration has happened, however, new spatial data sources can uncover the place to where people have migrated. Injustice in accessing data where some people have access to data while others don’t is also a limitation. Problems also arise in data linkages and integration (e.g. unidentifiable people in some datasets). Returning to the usage of commercial data from industries for research purposes, sensitivities of data (e.g. location data) are now more spread among people, which made the number of people opting-out from sharing their data higher. This in turn increases the representation bias in the industry data, making it less suitable for revealing demographic processes.

Finally, the plenary ended with some suggestions for future research. Interdisciplinary research emerging from multidisciplinary teams coming together and bringing ideas from different disciplines (eg merging spatial data with tropical medicine with demography data) would be interesting. Despite the various challenges faced with existing data, population science and demography have lots of potential. The ways demographers analyse population data have changed across time because people are changing. They first started by putting people in the numerator to people self-identifying to considering ethnicity and gender dimensions. Analysis will always be socially constructed and there will always be problems to find solutions for.

Second Plenary Session: "Measuring Populations and their Characteristics: Past, Present and Future"

Professor Sir Ian Diamond (National Statistician)

Sir Ian Diamond began his plenary talk by reminding conference attendees that counting the population has a long history in England and Wales. William Pitt Morton collected information about the people where he lived in Dorset in the nineteenth century and conducted a census of the parish of Corfe Castle and understood the power and value of information on individuals when used together. The first estimates or counts for England and Wales come from the 1841 Census. In the early years, the focus of the census was on counts of the population. Sir Ian went on to explain that in more recent years, there has been a move from population counts to population estimates. The first strategy for under-enumeration was undertaken in 2001 and Sir Ian worked on the design of a census coverage survey for the 2001 Census to adjust for under-enumeration.

Moving forwards to the present, the aim of Census 2021 for England and Wales was to produce high quality, flexible, and accessible census statistics for users. There were a number of quality targets: a 94% overall response rate; at least 80% in every local authority; a 75% online response; and the minimisation of variability in responses. Quality assurance included a coverage survey, validation against comparators, top quality fieldwork and collaboration with local authorities. There were many successes in Census 2021: an outstanding engagement and publicity campaign; excellent management information; a digital-first questionnaire; and community and local authority engagement.

The Office for National Statistics (ONS) published the first census release on the 28th June 2022 where the population of England and Wales in 2021 was 59,597,300. The population had grown by 3.5 million since 2011, with 18.6% of the population aged 65 years and over. There was extensive news coverage: over 2,150 pieces of media coverage, 104 million social media users reached and over 10,000 stakeholders engaged. However, Sir Ian highlighted that while there is increasingly the need for more timely population estimates there are challenges to producing estimates between each census, and a need for greater granularity in the data. At the same time there is also the need to consider the costs of a full census.

Looking forward, ONS are working to produce admin-based migration statistics using new data sources. Sir Ian went on to raise wider questions, which are paramount in the population topic area, including: what do we mean by migration and movement in 2022? And are current definitions appropriate? Research has shown that immigration and emigration estimates can be improved by using advanced passenger information (API). ONS are working on a dynamic population model to produce more timely, frequent and coherent population estimates. With the cohort component method at its heart, it will have a formal statistical framework including a range of data sources, and structural coherence between population stocks and flows.

Beyond population estimation, Sir Ian outlined that ONS have also been carrying out research on individual and household characteristics, including exploring the use of administrative data to produce statistics on housing stock characteristics. This has been achieved by linking individual and household data to produce income estimates for lower super output areas. At the same time, ONS colleagues have developed initial subnational estimates on income by ethnicity from administrative data.

Looking to the future, ONS will use the best information to produce more frequent, timely and inclusive statistics about the population and its characteristics. They will provide insights that are coherent and flexible to evolving user needs. They want to provide quicker and more frequent population and migration statistics.

In summary, the need for governments to understand the spatial patterns of their populations, together with their demographic and socioeconomic characteristics, has never been greater. Through greater use of administrative data, ONS will provide accurate, frequent and timely statistics. Sir Ian concluded his talk with a quote from William Pitt Morton.

“From such returns great parochial advantages would be derived wheresoever they might be adopted, and if they were general great national benefit would result therefrom”.

Julian Buxton
Mary Abed Al Ahad
BSPS

Letter to the Editor

Sir,

In the Epilogue to my *Consciousness from Descartes to Ayer,* Palgrave Macmillan, 2021, I put forward an account of how human language was developed. I should like to briefly summarise my account, then use it to answer one of the great questions relating to Neanderthals and *Homo sapiens*, namely: Why did the Neanderthal become extinct, leaving us Sapiens as the only human species?

My thesis is that the Neanderthals became extinct because they could not learn the symbolic human language which had been developed by the hybrids, the offspring of the successful mating of Sapiens and Neanderthal, whereas the Sapiens were able to learn the human language from the hybrids, because of their ability to produce a greater range of articulate sounds.

Yet the Neanderthals helped to bring about the development, through their share in engendering the hybrids and, according to my hypothesis, in their bafflement at the sounds the Sapiens produced which they could not produce or understand. Therefore, without the Neanderthals, symbolic human language would not have come into being. But in another respect their contribution was not necessary, which is shown in the fact that the pure Sapiens, who had no Neanderthal genes, and did not migrate out of Africa, could learn the human language. Yet once the human language was developed by the hybrids and was being learned by the Sapiens, the Neanderthals, who in appearance were not greatly different from the Sapiens, would be becoming more and more different from Sapiens, as apes are from us.

Could a way have been found so that, given this strange difference and similarity, the two kinds of humans could both subsist? It seems not, but why? I think because the Neanderthals were in a vulnerable position, more so in respect of Sapiens than apes, and for at least two reasons. First because apes are not in such direct competition for the same foods and lodging as the Neanderthals; and secondly because the Neanderthals were not as strong as apes. This then is my explanation of why they became extinct.

David Berman
Philosophy Department
Trinity College Dublin

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The Adelphi PhD project 2023-2026

In 2022 the Council of Adelphi Genetics Forum (AGF) debated and adopted the proposal to offer funding for a PhD studentship to be supervised in a UK university. One of AGF's chief aims is to promote research and discussion concerning the scientific and societal understanding of human heredity. We are also eager to address representation of students and researchers from minority ethnic or disadvantaged backgrounds. It was felt that by supporting a UK student for three years to explore a topic that resonates strongly and clearly with these aims would be a good aim.

The project was advertised as widely as possible. The requested information was kept brief: 500-word project description with title, aims and approach, including outreach plans; details the supervising team, preferably with complementary skills; departmental and university support structures; brief details of the recruitment process with the aim of targeting the desired student pool. An eight-member assessment panel with suitable expertise was set up from Council. Council members were not eligible to apply. Conflicts of interest were declared. Preliminary independent scores from each panel member were gathered and all the applications were then discussed in detail. Making the final decision was difficult as several excellent projects were submitted. We wished we had sufficient funds to select more than one proposal. The selected project involves two co-supervisors, Adam Rutherford and Mark Thomas from the Department of Genetics, Evolution and Environment at UCL. On the next page they present their aims and plans for the three-year project.

Veronica van Heyningen
Honorary Professor University of Edinburgh and UCL

There is a problem at the heart of population genetics, right there in its name. It's a field that evolved in the early 20th century, with the work of J.B.S. Haldane, Sewall Wright and Ronald Fisher, as they attempted to use maths to reconcile emerging knowledge of genes, with the Darwinian processes of evolution. Population genetics became the central pillar of the Modern Synthesis of evolutionary biology. Since then, spectacular progress has been made in establishing theoretical frameworks for the evolution of natural populations.

But during the laying of these foundations, computational power was limited to pen and paper, and DNA was yet to be discovered as the molecule that bears genetic information. And so, constraints were imposed upon how we model nature. The most significant of these was the very concept of the population. For reasons of mathematical convenience, the Modern Synthesisers necessarily assumed that populations should be considered as discrete groups of panmictic (random mating) organisms. In the real world no such population has ever existed.

Instead, in nature, organisms move in time and space and mate with those who are closer, even when there are geographical constraints, such as life on an island. Our project for the Adelphi Studentship is entitled 'Removing the population concept from population genetics', and will look at multiple aspects of the foundation and legacy of this mathematical convenience at the heart of our field. We want to account for the impact that this type of modelling has had on our understanding of evolution, especially as now we have a dramatic increase in the volume of available genetic data, and powerful computational and statistical techniques. The concept of the population has also reified outdated and unscientific concepts such as 'race' and dominates the rapidly expanding 'Direct to the Consumer Genetic Ancestry Testing' industry, which has fuelled outmoded racialized views of human genetics and origins in the public domain. We want to build a living history for working scientists to come together and move away from the legacy of prioritising mathematical conveniences over the explanatory power of models that better reflect reality.

We have recruited a student, and are waiting for the ink to dry on their paperwork, with the plan to start work in September 2023. They will report back to Adelphi as soon as we're up and running.

Adam Rutherford
University College London

ADELPHI GENETICS FORUM

Conference 2023

Population diversity, its biological consequences and impact on disease risk

The Royal Society
18 October, 2023

It has long been known that people not only differ in DNA sequence from each other- (any two people plucked at random differ by the order of 0.1% of their DNA bases), but the frequencies of many of the nucleotide changes differ in different parts of the world. This means that people living within the same geographic areas or societal groups tend to cluster together as a result of their shared ancestry, while those living further apart may form distinguishable clusters. But migration of peoples leads to admixture, and also differing non-genetic factors in different parts of the world may lead to differential selection and thus also differences in gene frequency. So, our genetic history is complex. This conference attempts to address the extent and functional significance of this diversity. Talks will cover population history, single gene disorders and selection, disease susceptibility, pharmacogenetics and the challenges of precision medicine.

Admission is free but strictly by ticket from:
www.eventbrite.co.uk
or *The General Secretary at:*
executiveoffice@adelphigenetics.org